



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HU, JING-SHAN
OLSEN, HENRIK S.
ROSEN, CRAIG A.

(ii) TITLE OF INVENTION: HUMAN VASCULAR ENDOTHELIAL GROWTH FACTOR 3

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
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(C) CITY: WASHINGTON
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/033,662
(B) FILING DATE: 03-MAR-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/469,641
(B) FILING DATE: 06-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1488.1040001

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AGA AGG TGT AGA ATA AGT GGG AGG CCC CCG GCG CCC CCC GGT GTC	48
Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val	
1 5 10 15	
CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC CAG AGG	96
Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg	
20 25 30	
AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC CAG CCC	144
Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro	
35 40 45	
CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC GTG GCC	192
Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala	
50 55 60	
AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT GGC TGC	240
Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys	
65 70 75 80	
TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC CAA GTC	288
Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val	
85 90 95	
CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG GGG GAG	336
Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu	
100 105 110	
ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA AAA AAG	384
Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys	
115 120 125	
GAC AGT GCT GTG AAG CCA GAC AGG GCT GCT ACT CCC CAC CAC CGT CCC	432
Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro	
130 135 140	
CAG CCC CGT TCT GTT CCG GGC TGG GAC TCT GCC CCC GGA GCA CCC TCC	480
Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser	
145 150 155 160	
CCA GCT GAC ATC ACC CAA TCC CAC TCC AGC CCC AGG CCC CTC TGC CCA	528
Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro	
165 170 175	
CGC TGC ACC CAG CAC CAC CAG TGC CCT GAC CCC CGG ACC TGC CGC TGC	576
Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys	
180 185 190	
CGC TGT CGA CGC CGC AGC TTC CTC CGT TGT CAA GGG CGG GGC TTA GAG	624
Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu	
195 200 205	
CTC AAC CCA GAC ACC TGC AGG TGC CGG AAG CTG CGA AGG TGA	666
Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val
 1 5 10 15
 Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg
 20 25 30
 Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro
 35 40 45
 Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala
 50 55 60
 Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys
 65 70 75 80
 Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val
 85 90 95
 Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu
 100 105 110
 Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
 115 120 125
 Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
 130 135 140
 Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser
 145 150 155 160
 Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro
 165 170 175
 Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys
 180 185 190
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
 195 200 205
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 210 215 220

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
GCATGGATCC CAGCCTGATG CCCCTGGCC 29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
GCATTCTAGA CCCTGCTGAG TCTGAAAAGC 30

(2) INFORMATION FOR SEQ ID NO:5:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
GACTGCATGC ACCAGAGGAA AGTGGTGTC 29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
GACTAGATCT CCTTCGCAGC TTCCGGCAC 29

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
130 135 140
Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
145 150 155 160
Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His
165 170 175
Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr
180 185 190

Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys
195 200 205

Arg Cys Asp Lys Pro Arg Arg
210 215

C6